

FIG. 1A

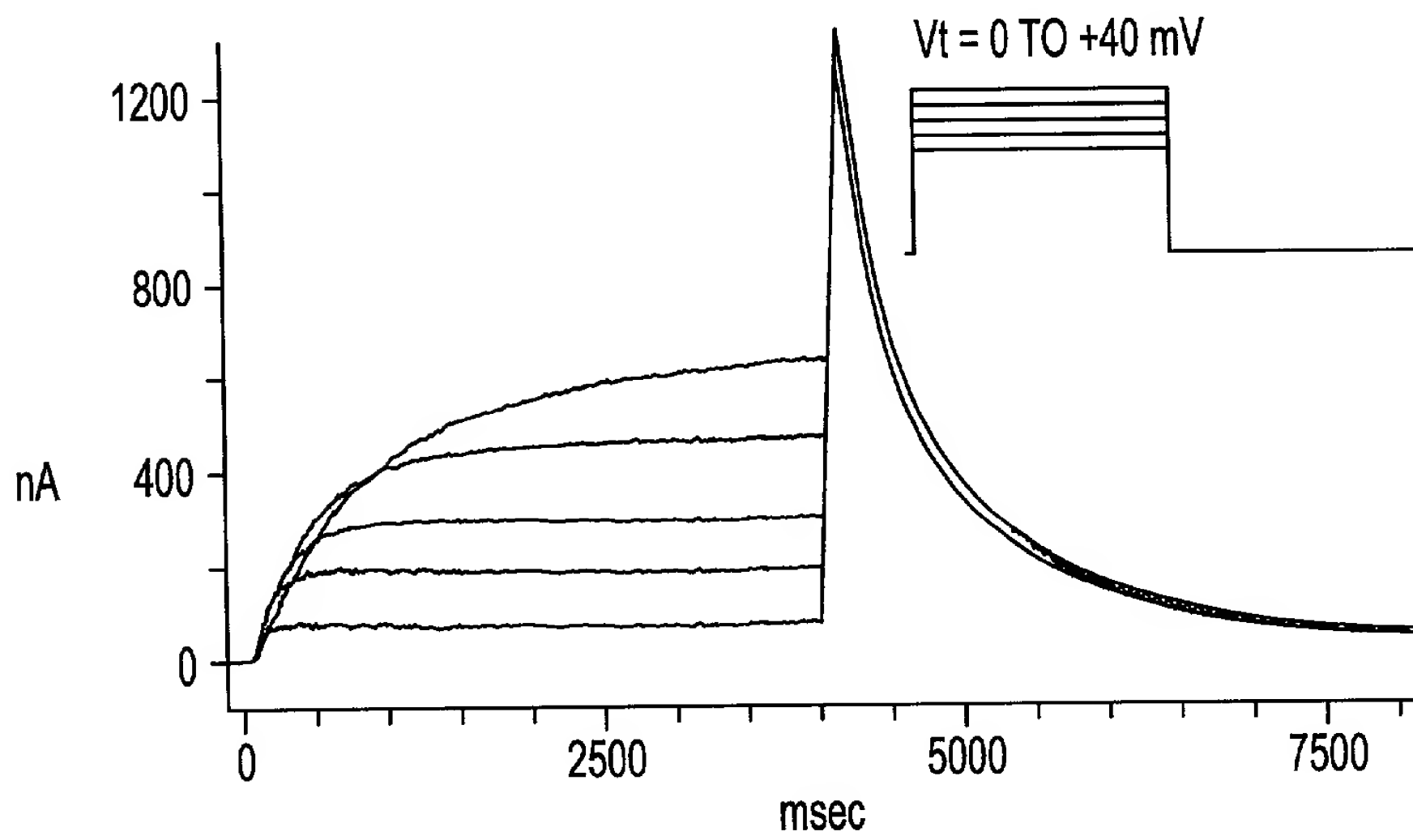


FIG. 1B

004147-56656260

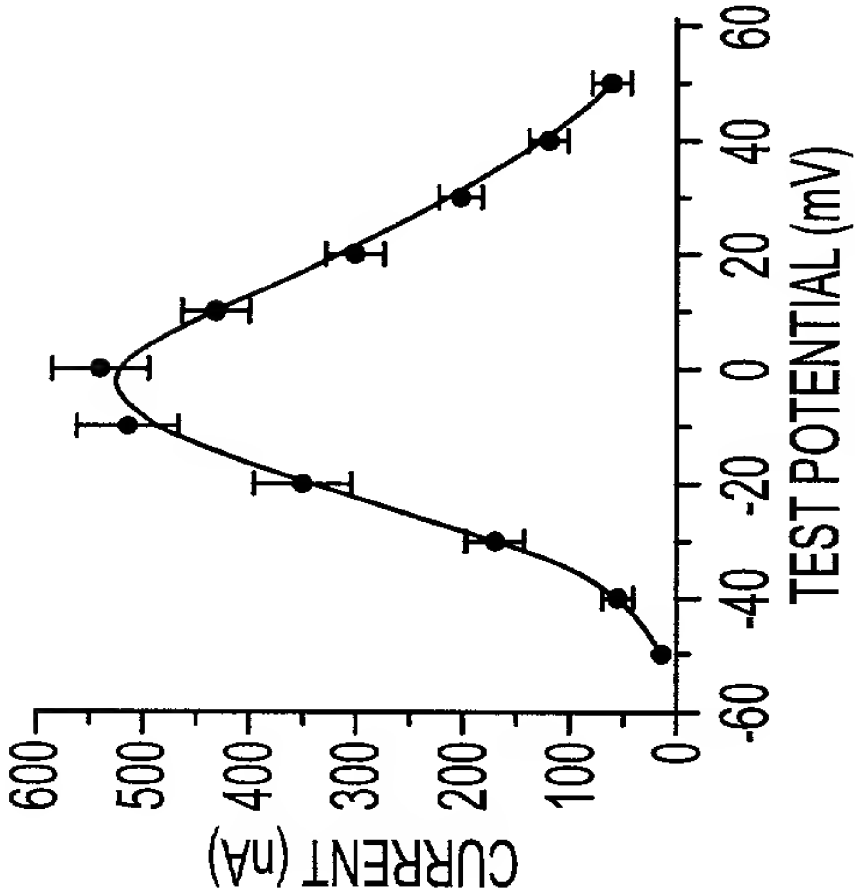


FIG. 1C

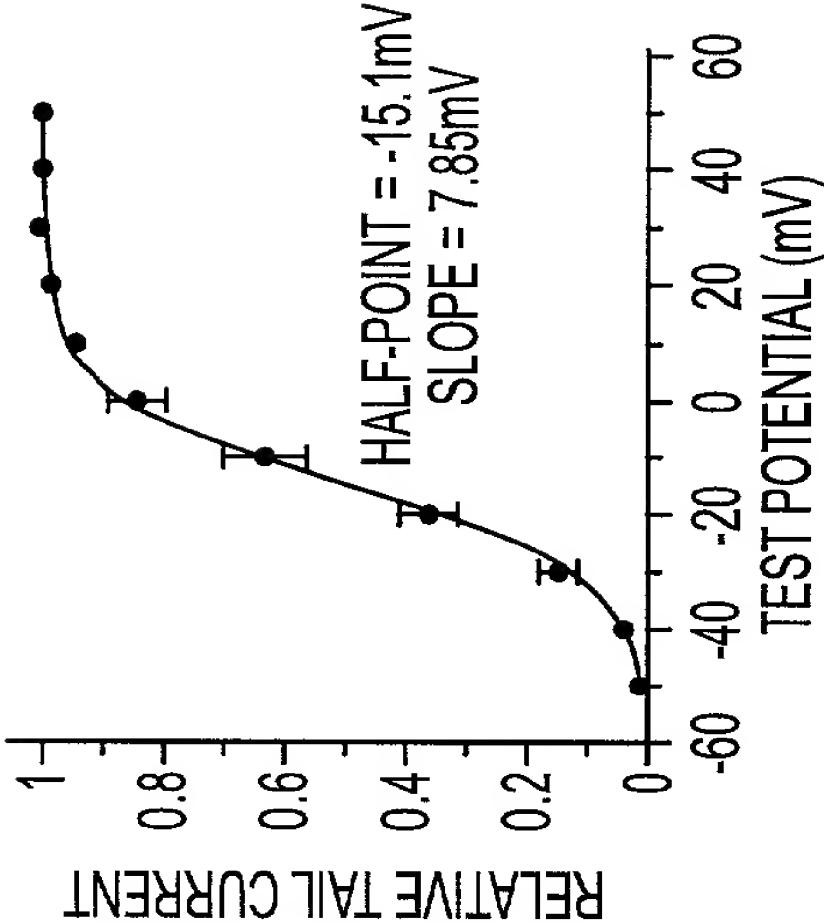


FIG. 1D

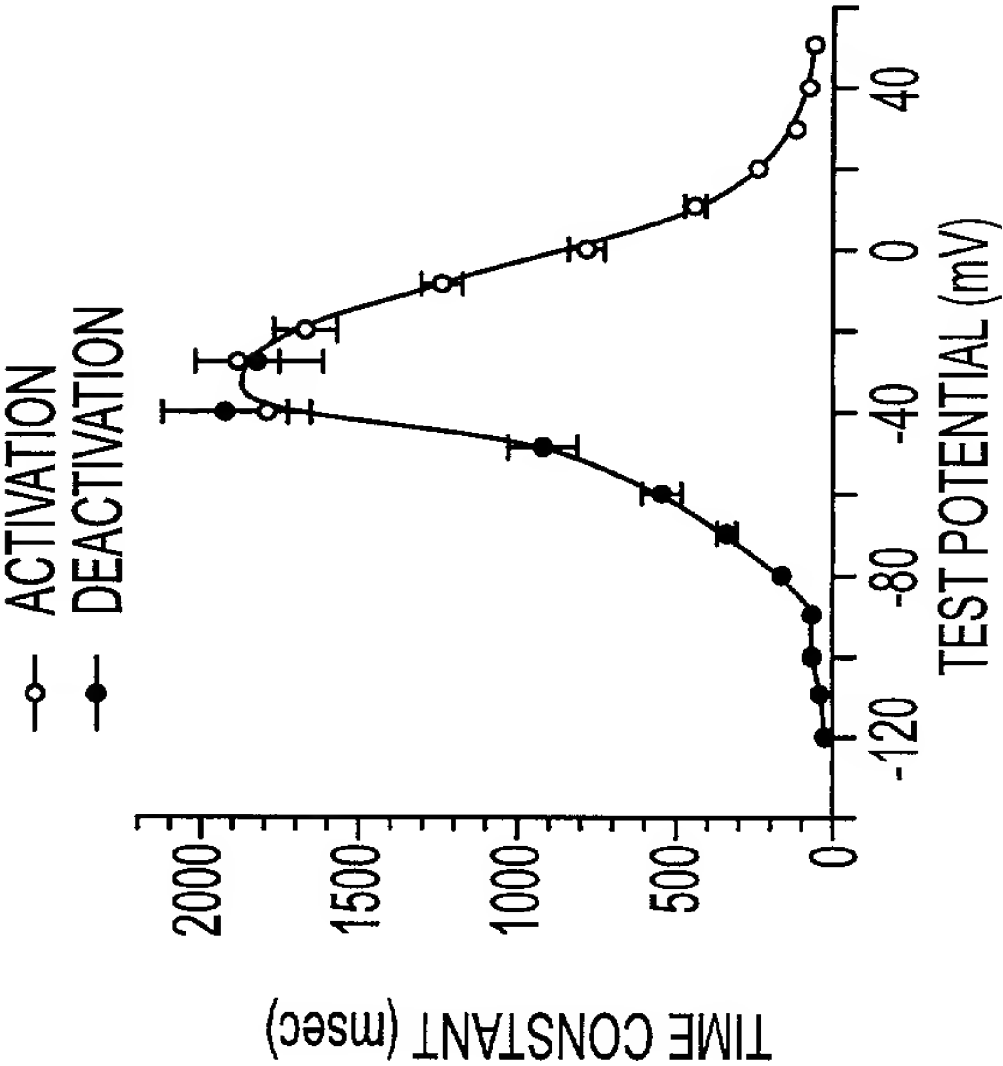


FIG. 2C

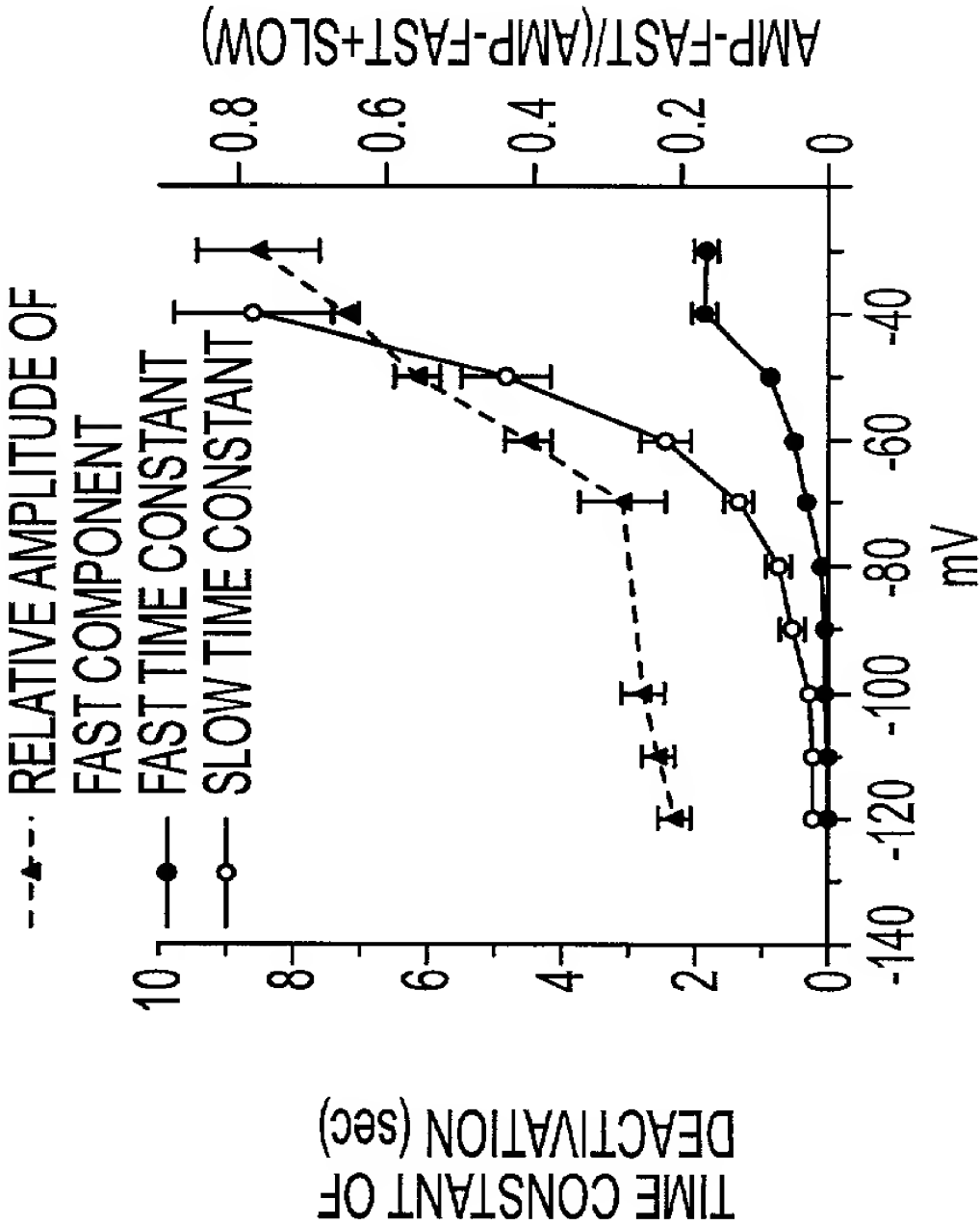


FIG. 2D

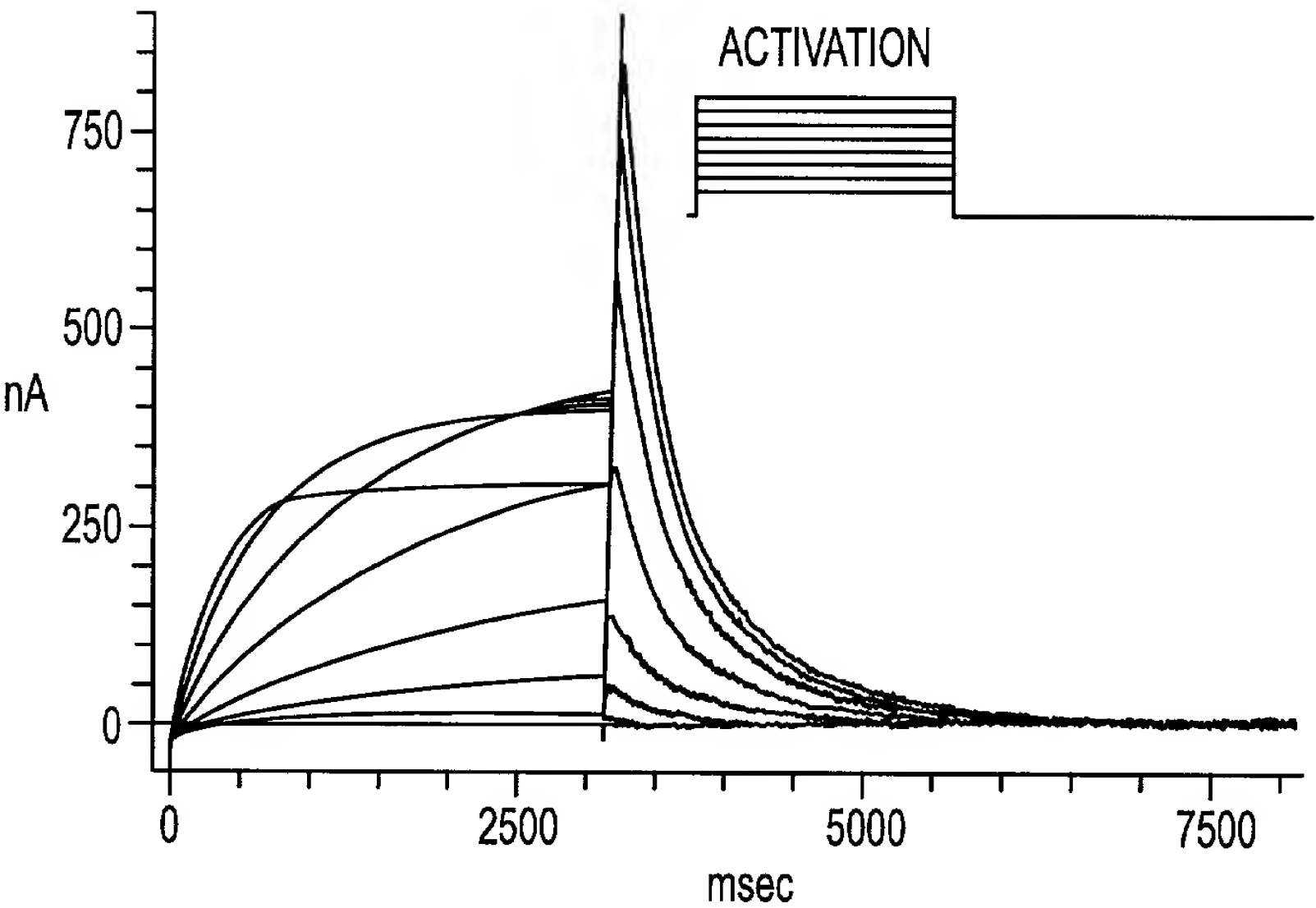


FIG. 2A

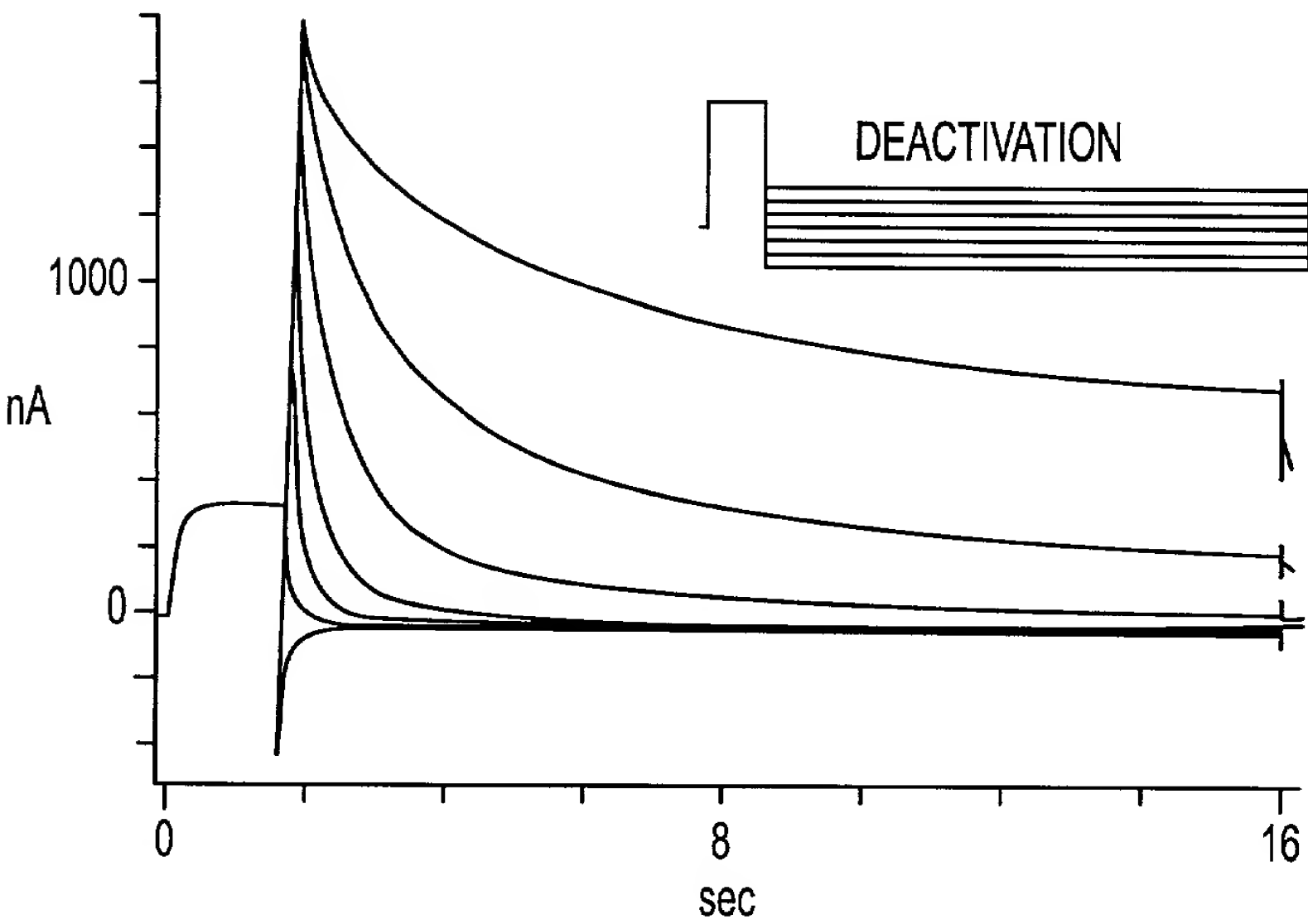


FIG. 2B

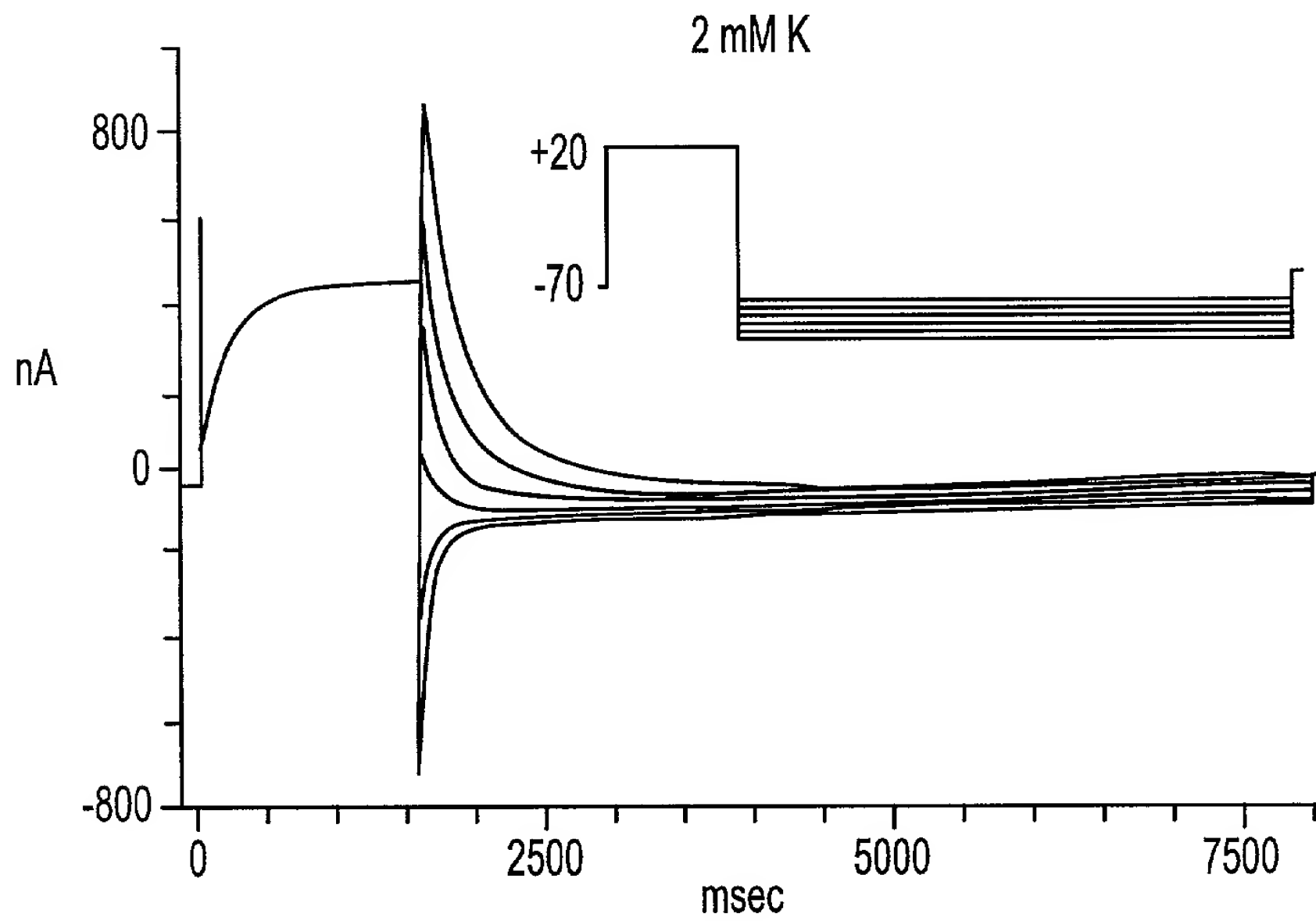


FIG. 3A

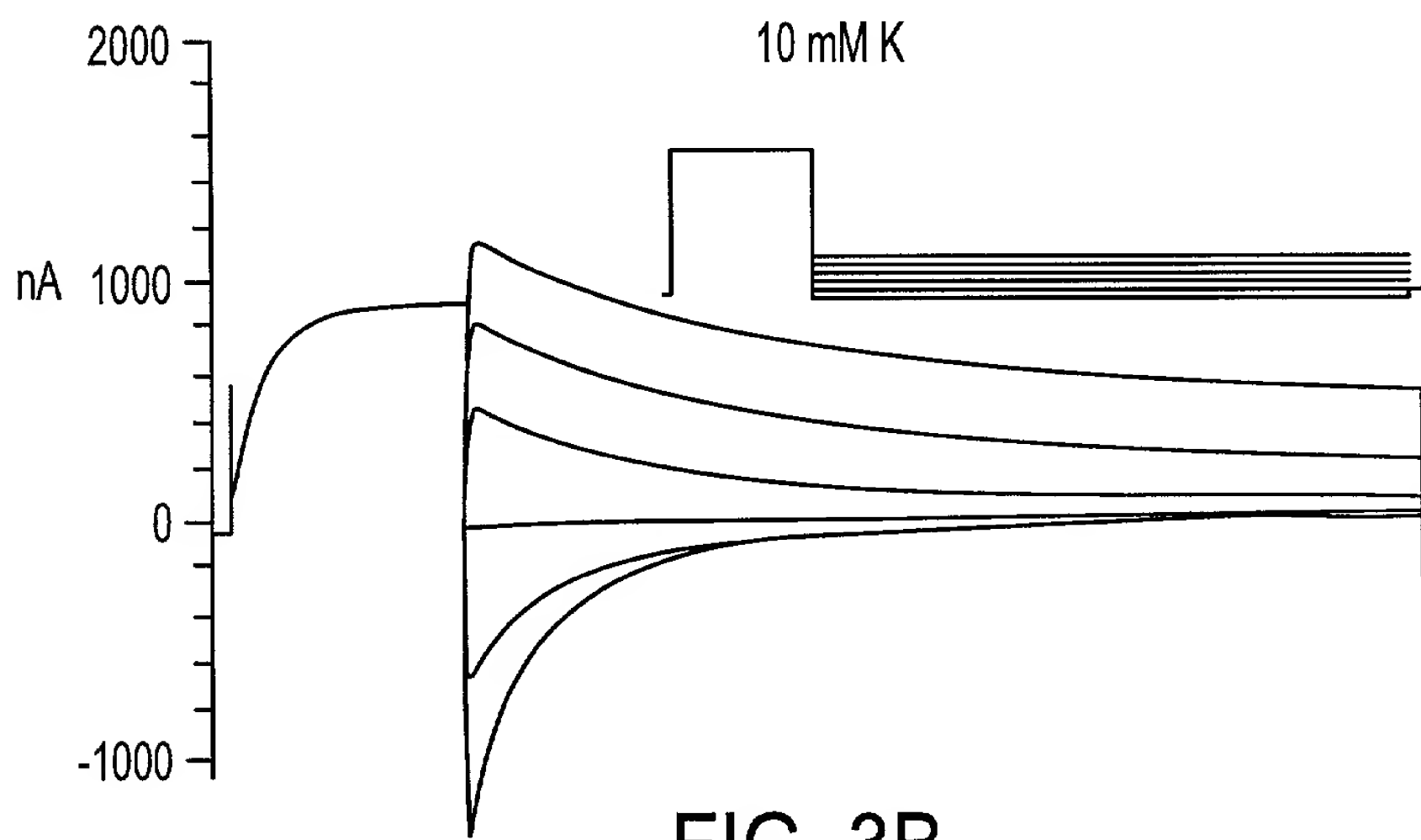


FIG. 3B

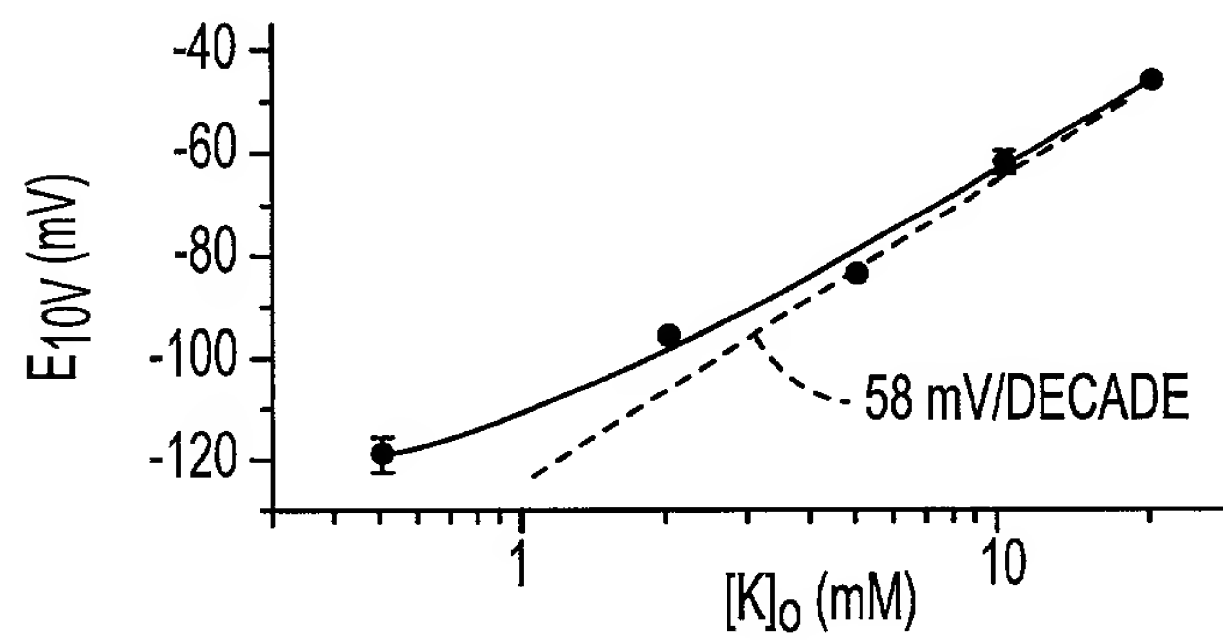


FIG. 3C

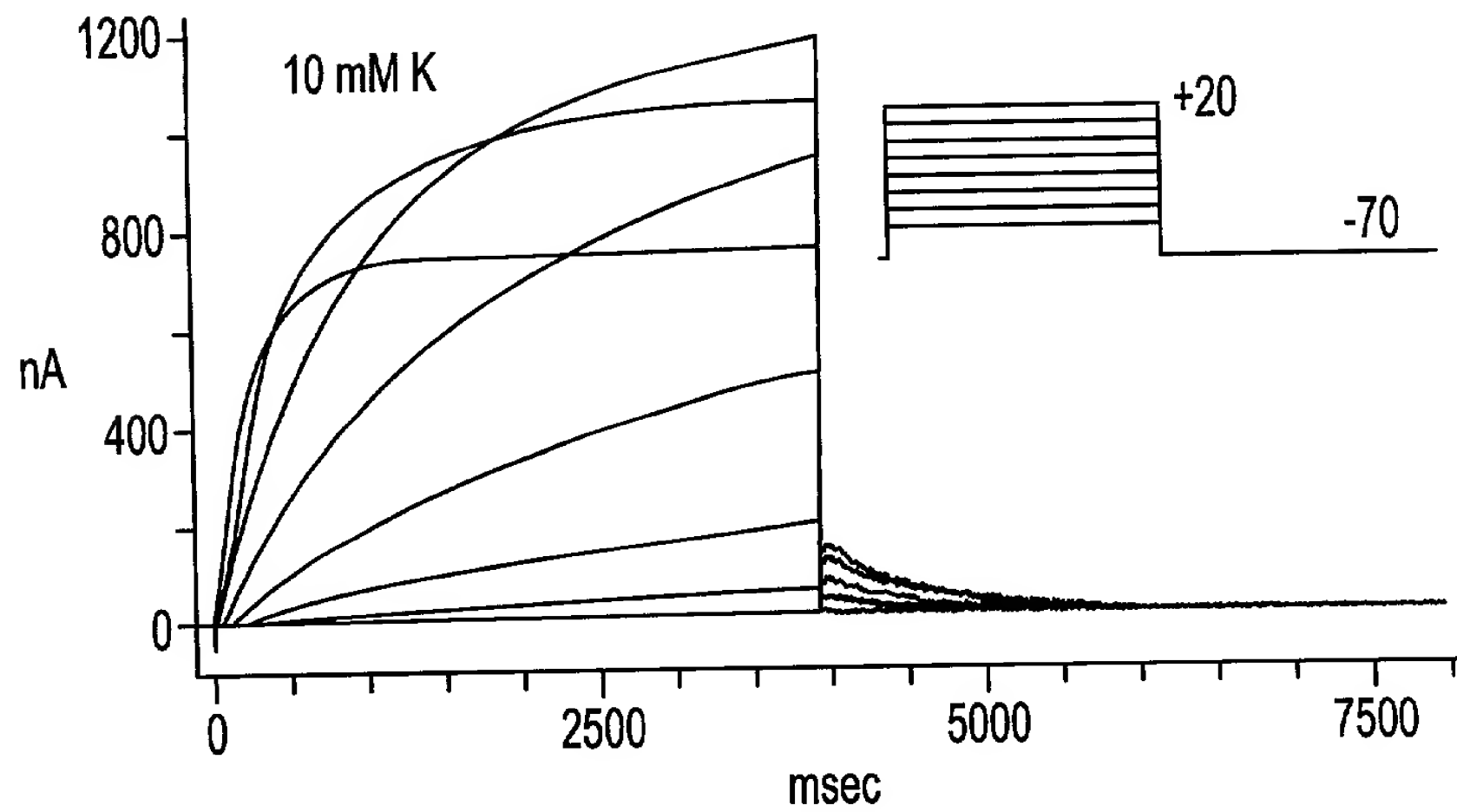


FIG. 4A

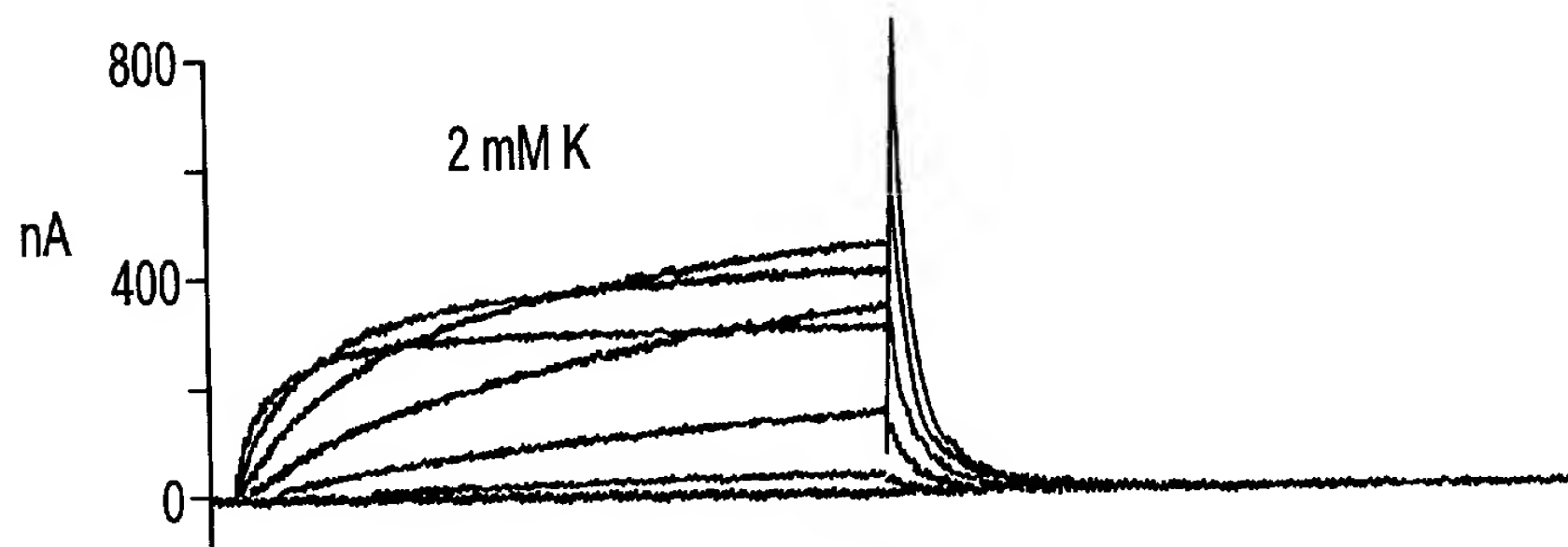


FIG. 4B

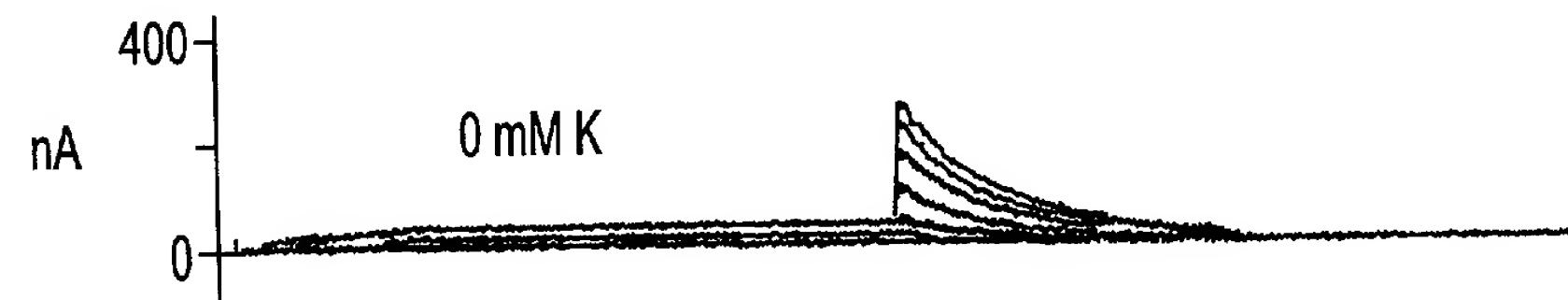


FIG. 4C

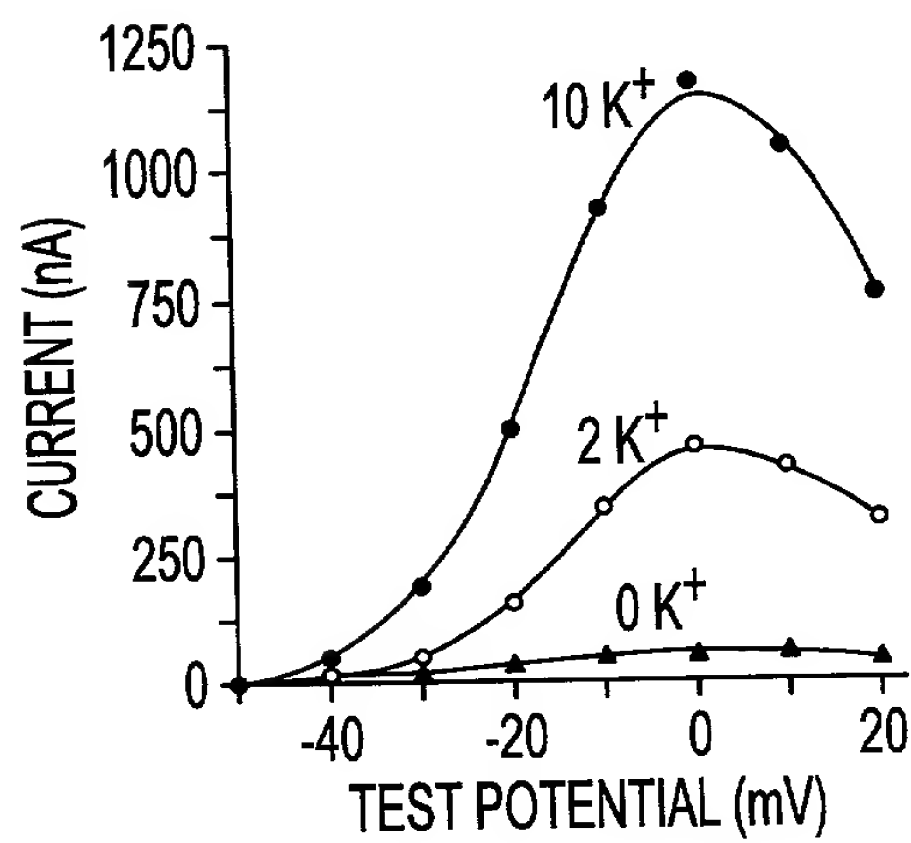


FIG. 4D

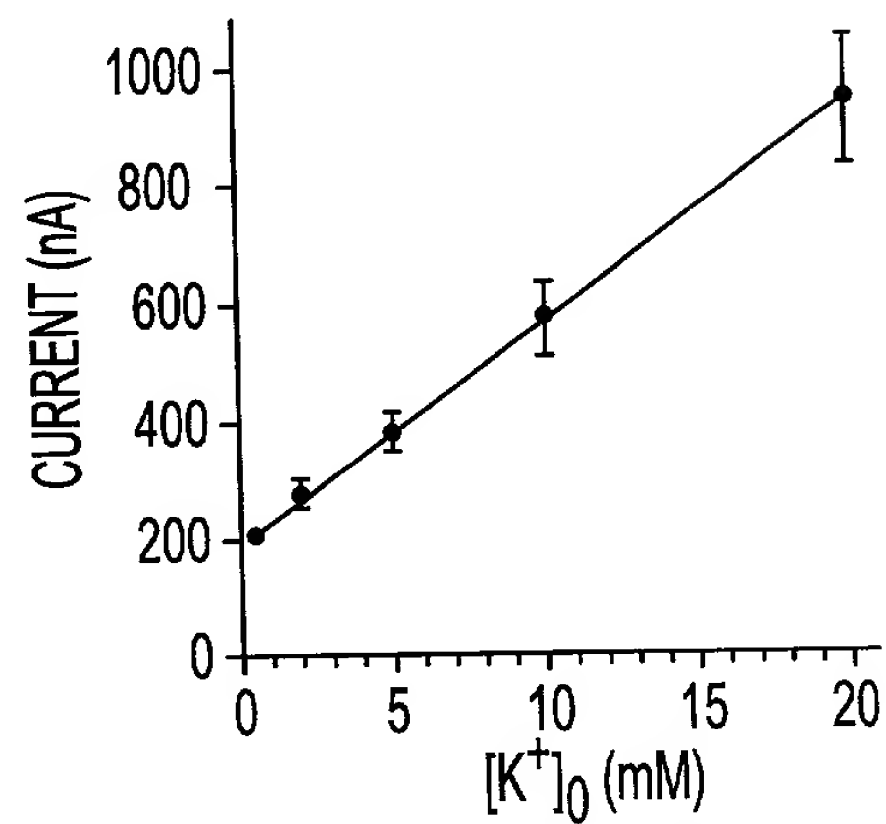
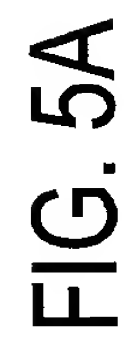


FIG. 4E

001121-5665E/60



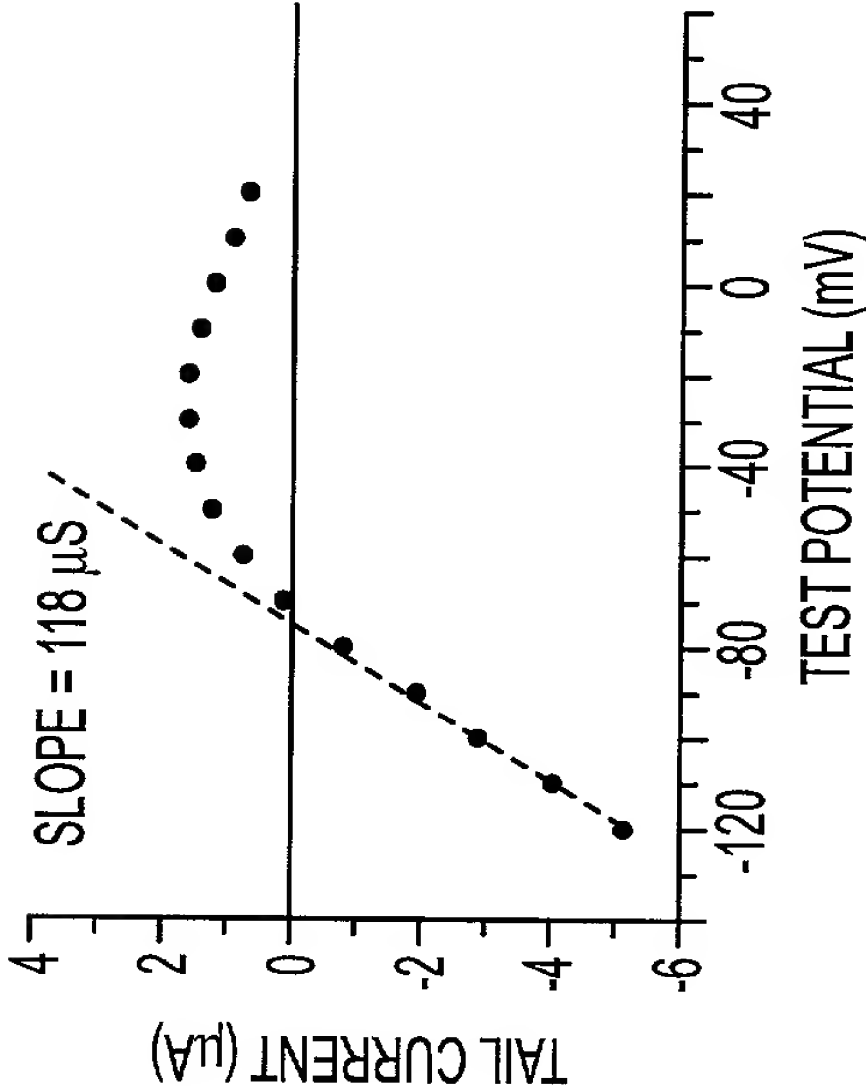


FIG. 5C

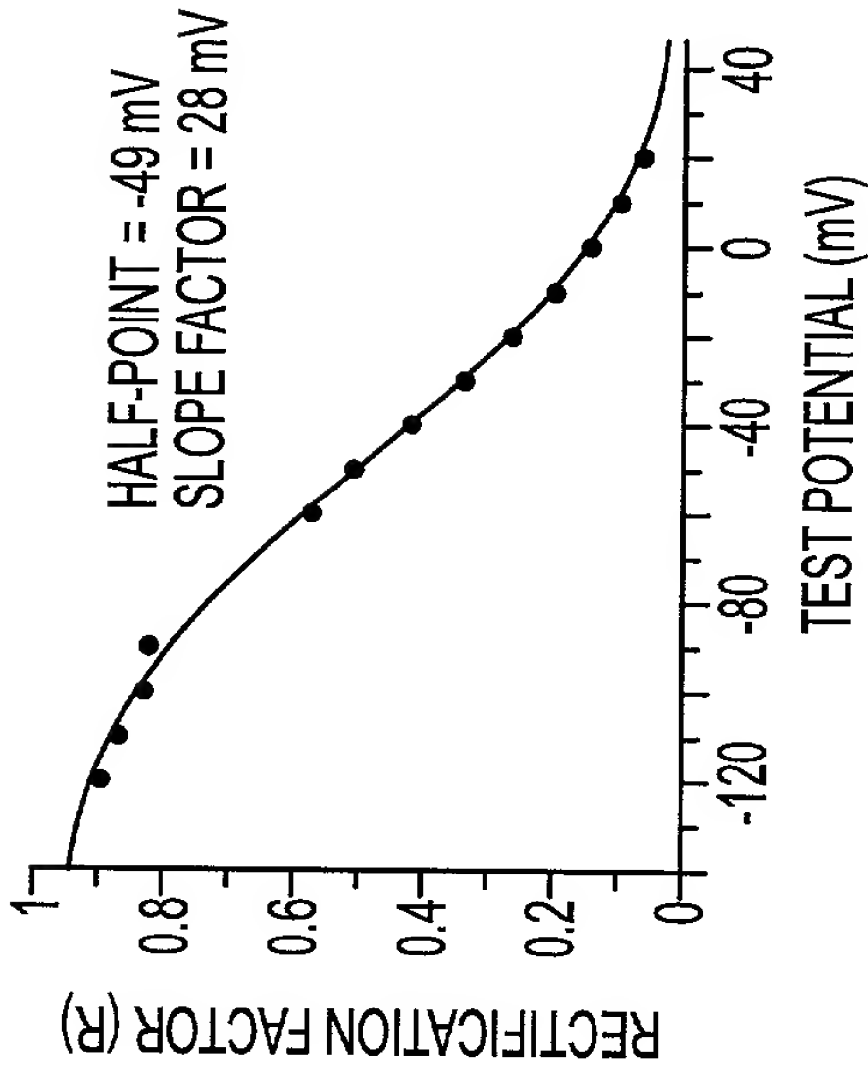


FIG. 5D

FIG. 6A

FIG. 6B

FIG. 6C

FIG. 6D

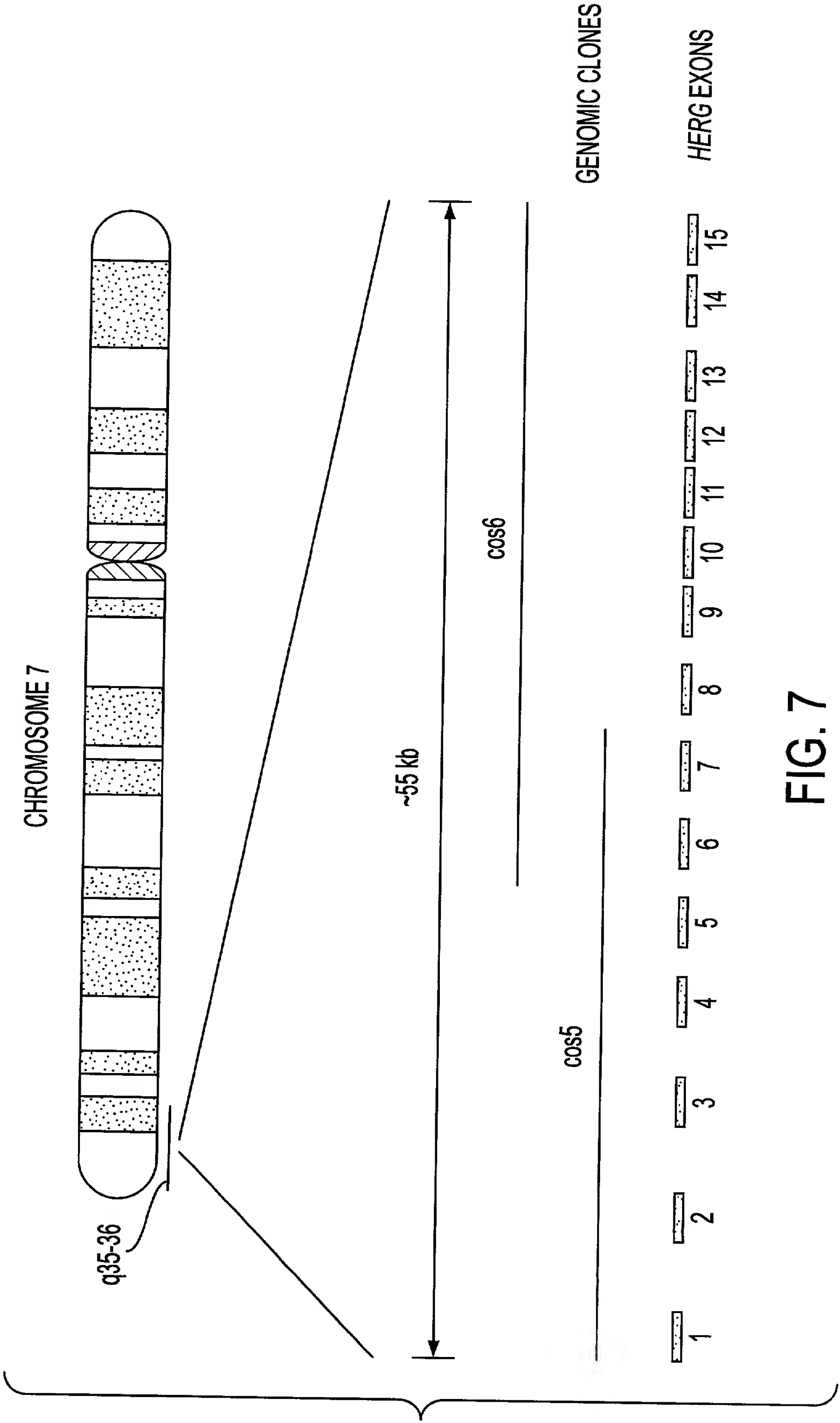


FIG. 8A

[illegible]

AGCATCTTCGGCAACGTGTCGGCCATCATCCAGCGGCTGTACTCGGGCACAGCCCCTACCACACACAGATGCTGCGGGTG-2106
S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTCATCCGCTTCCACCAGATCCCCAATCCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCCTGGTCCTAC-2187
R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268
T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734
TCACTGCTGCAGCACTGCAAACCCTTCCGAGGGGCCACCAAGGGCTGCCTTCCGGGCCCTGGCCATGAAGTTCAAGACCACA-2349
S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761
CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACCGCCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430
H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511
I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

cNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592
G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673
D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869
GGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGCTTCCGCGAGCGCACGGAC-2754
G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGGACACGGAGCAGCCAGGGGAGGTGTCGGCCTTGGGGCCGGGCGGGGCGGGGCGAGGCGGAGTAGCCGGGGCCGGCCG-2835
K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923
GGGGGGCCGTGGGGGAGAGCCCGTCCAGTGGCCCTCCAGCCCTGAGAGCAGTGAGGATGAGGGCCAGGCCGAGCTCC-2916
G G P W G E S P S S G P S S P E S S E D E G P G R S S -950
AGCCCCCTCCGCTGGTGGCCTTCTCCAGCCCCAGGCCCCCGGAGAGCCCGGGTGGGAGCCCCCTGATGGAGGACTGC-2997
S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCCTGTCAGGCGCCTTCTCAGGAGTGTCCAACATTTTCAGCTTCTGGGGGGACAGT-3078
E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004
CGGGGCGCCAGTACCAGGAGCTCCCTCGATGCCCCGCCCCACCCCCAGCCTCCTCAACATCCCCCTCTCCAGCCCCGGT-3159
R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240
R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058
GACATGGCACTGTCCTGCAGCTGCTACAGAGGCAGATGACGCTGGTCCCGCCCCCTACAGTGCTGTGACCACCCCGGGG-3321
D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCCTCACCTTGGACTCGCTTTCTCAGGTTTCC-3402
P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112
CAGTTCATGGCGTGTGAGGAGCTGCCCCGGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCCTCTCCCTACCG-3483
Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139
GGCCAGCTGGGGGCCCTCACCTCCCAGCCCCTGCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCAGTGTGG-3564
G Q L G A L T S Q P L H R H G S D P G S * -1159
ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCGCTCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645
GGGAGAGGAACGAAAGCACAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAGAG-3726
GGGCAGGGGAGGGCCGCGAGTAGGTGGGGCCTGTGGTCCCCCACTGCCCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807
GGCACCCGGCCCTGGGCCTTAGGCACCTCAAGGACTTTTCTGCTATTACTGCTCTTATTGTTAAGGATAATAATTAAGGA-3888
TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTATCCTGAGGAG (A)n -3949

FIG. 8B



FIG. 9B

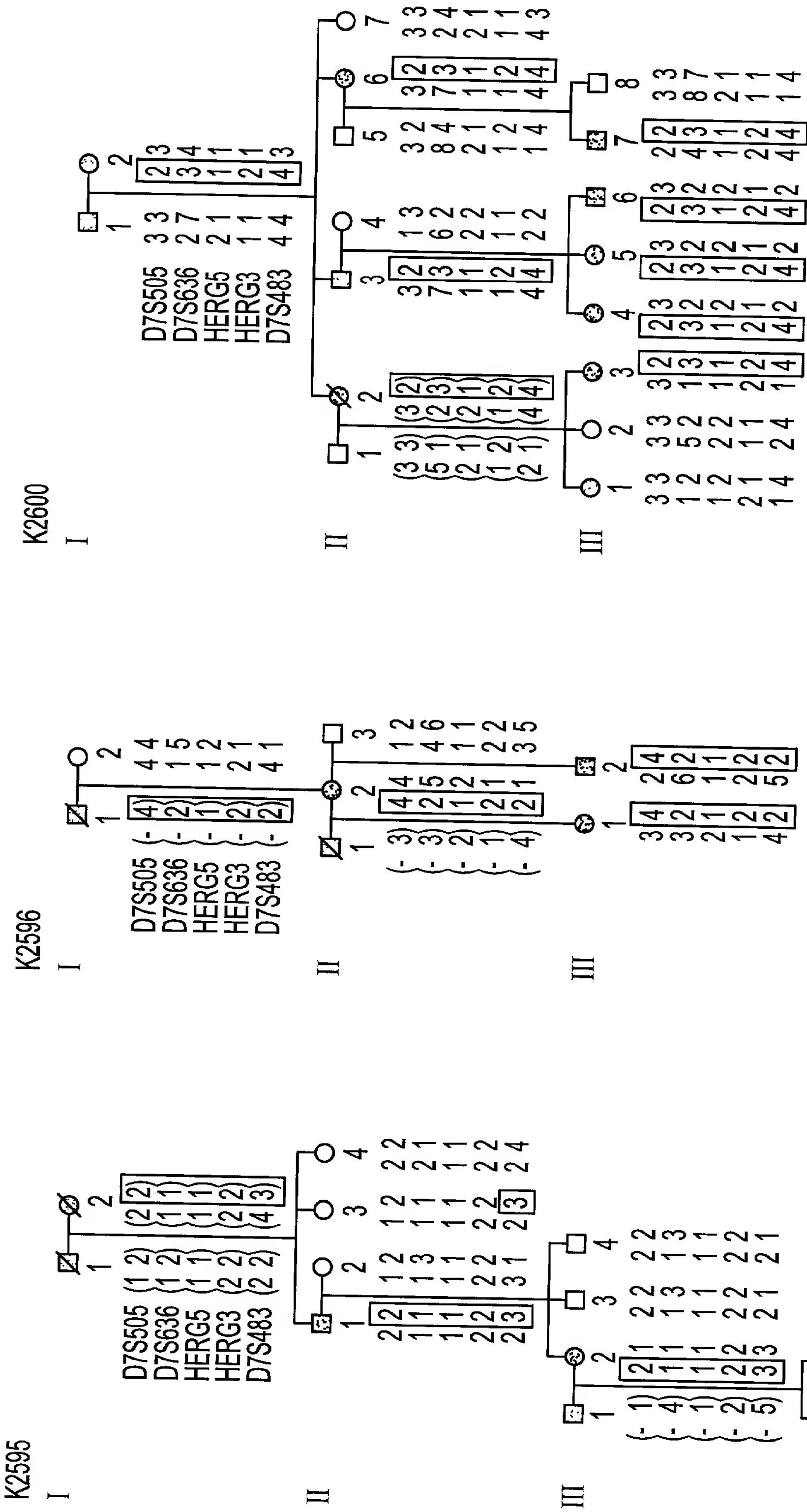


FIG. 9D

FIG. 9E

FIG. 9C

CONFIDENTIAL

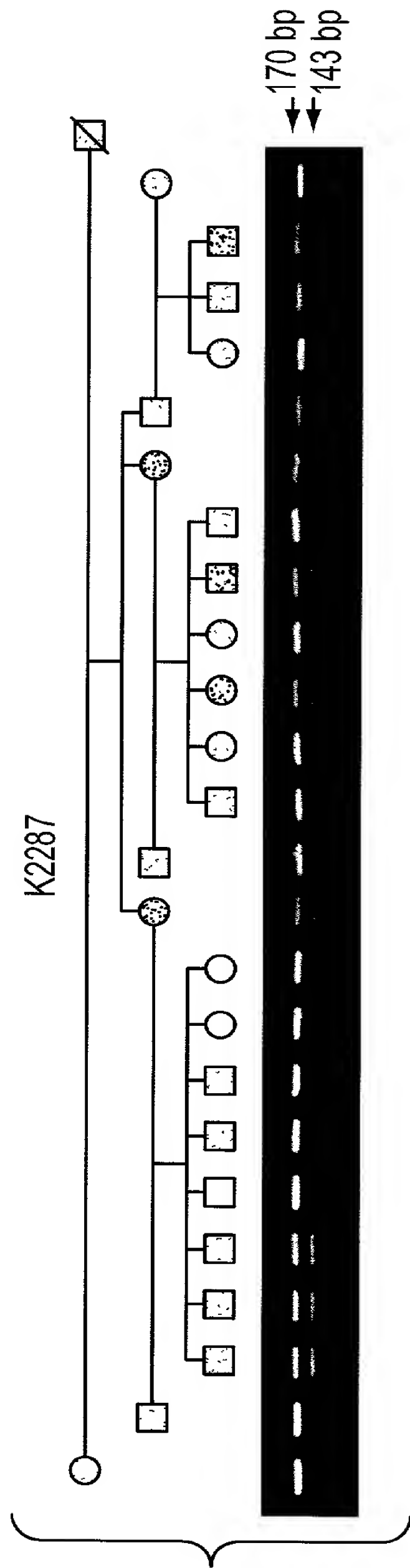


FIG. 10A

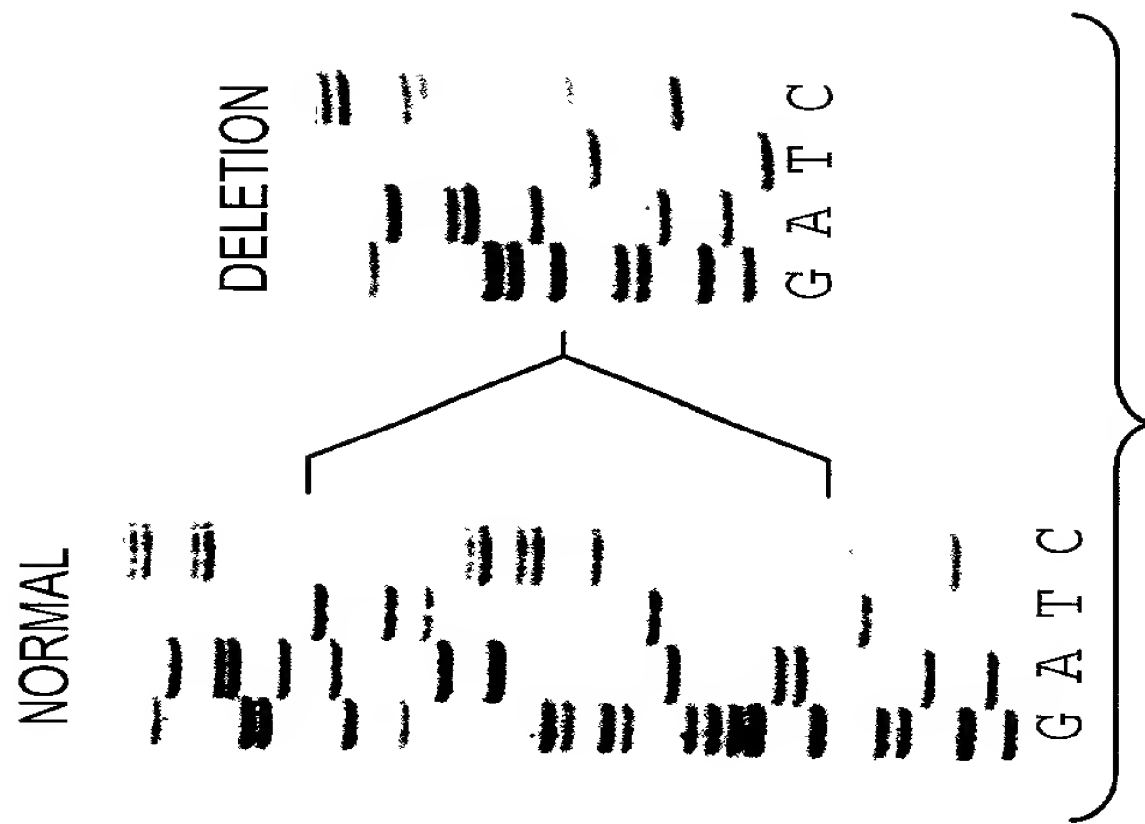


FIG. 10B

004467-9656/60

TGG	TTC	CTC	ATC	GAC	ATG	GTG	GCC	GCC	ATC	CCC	TTC	GAC	CTG	CTC	SEQ ID NO:96
W	F	L	I	D	M	V	A	A	I	P	F	D	L	L	SEQ ID NO:97
<div><div></div><div>S3</div><div></div></div>															

FIG. 10C

NORMAL	GTC	ATC	TAC	ACG	GCT	GTC	TTC	ACA	CCC	TAC	TCG	GCT	GCC	TTC	CTG	CTG	AAG	GAG	SEQ ID NO:98
	V	I	Y	T	A	V	F	T	P	Y	S	A	A	F	L	L	K	E	SEQ ID NO:99
DELETION	GTC	ATC	TAC	CGG	CTG	TCT	TCA	CAC	CCT	ACT	CGG	CTG	CCT	TCC	TGC	TGA			SEQ ID NO:100
	V	I	Y	R	L	S	S	H	P	T	R	L	P	S	C				SEQ ID NO:101

FIG. 11C

004737-56656260

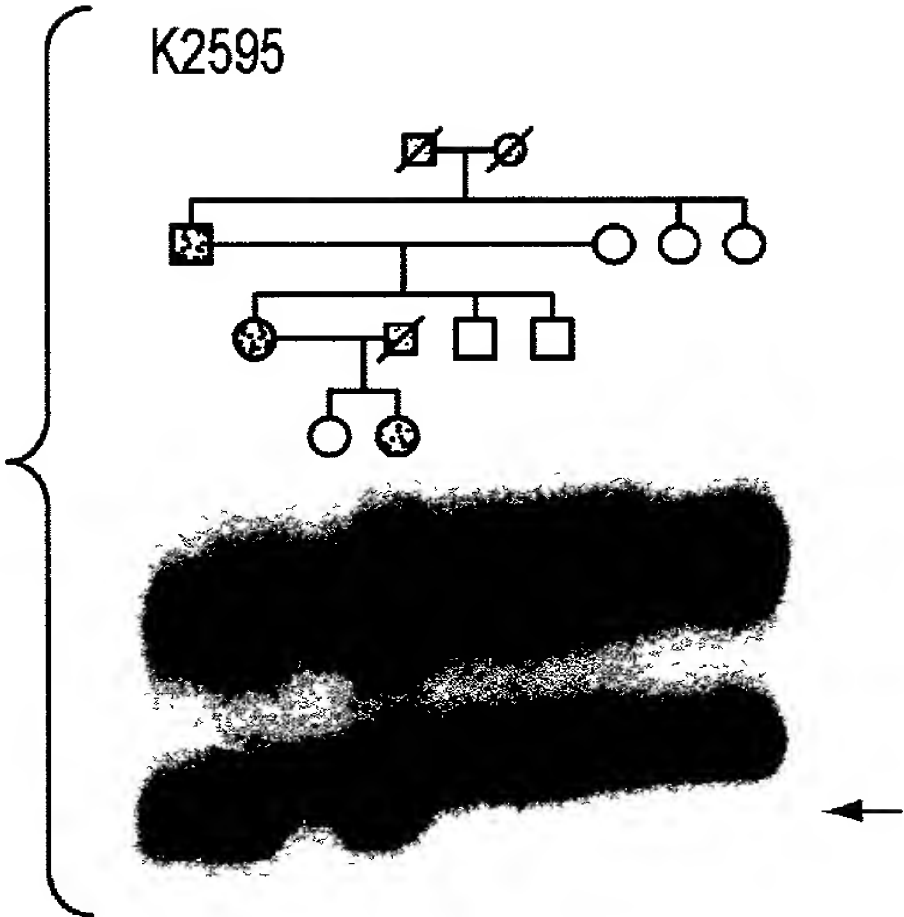


FIG. 11A

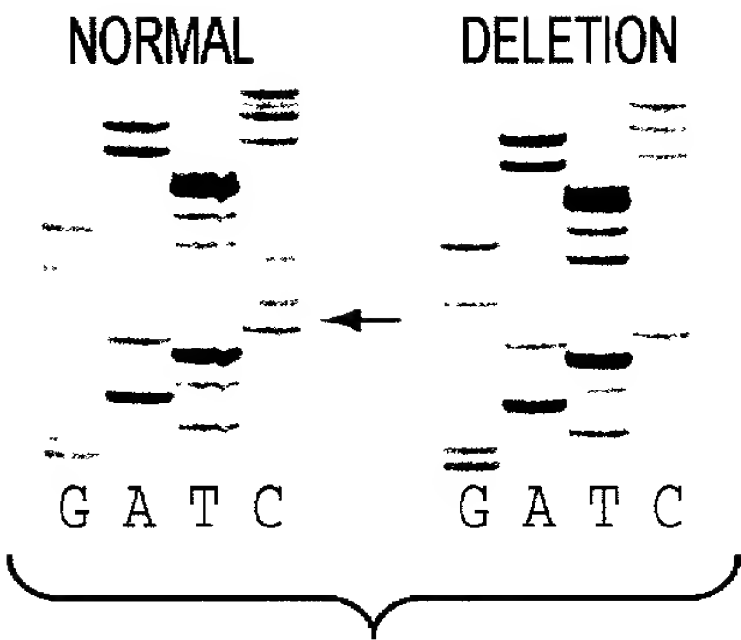
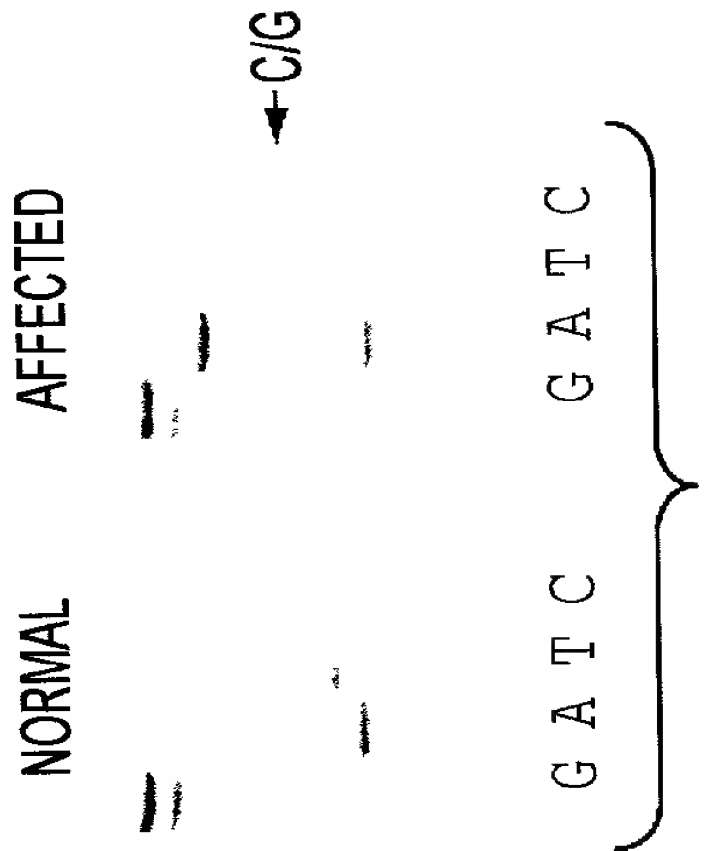
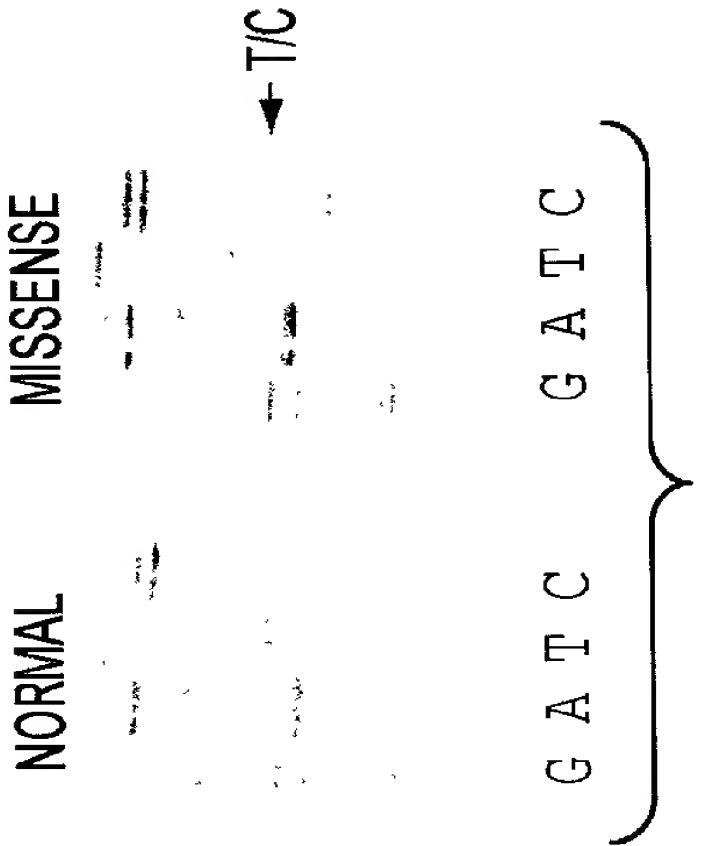
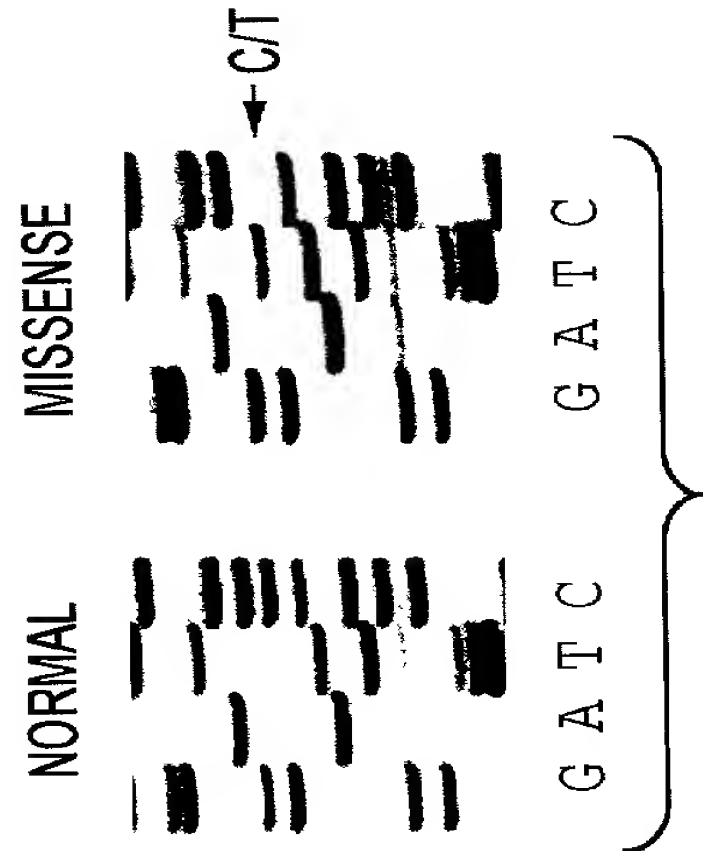
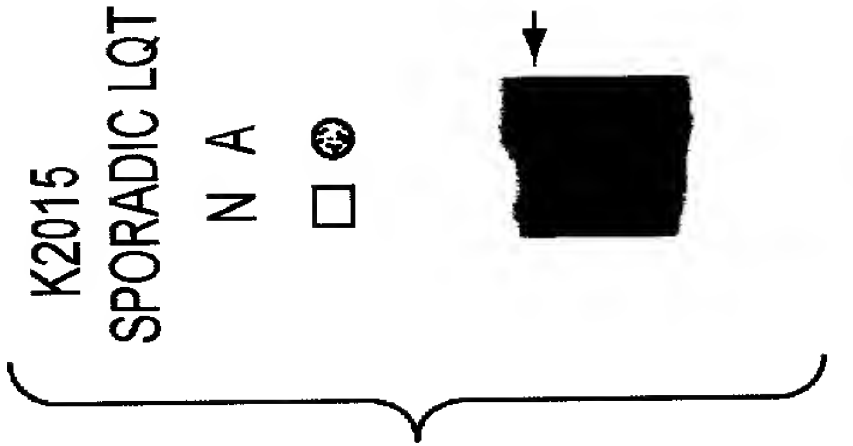
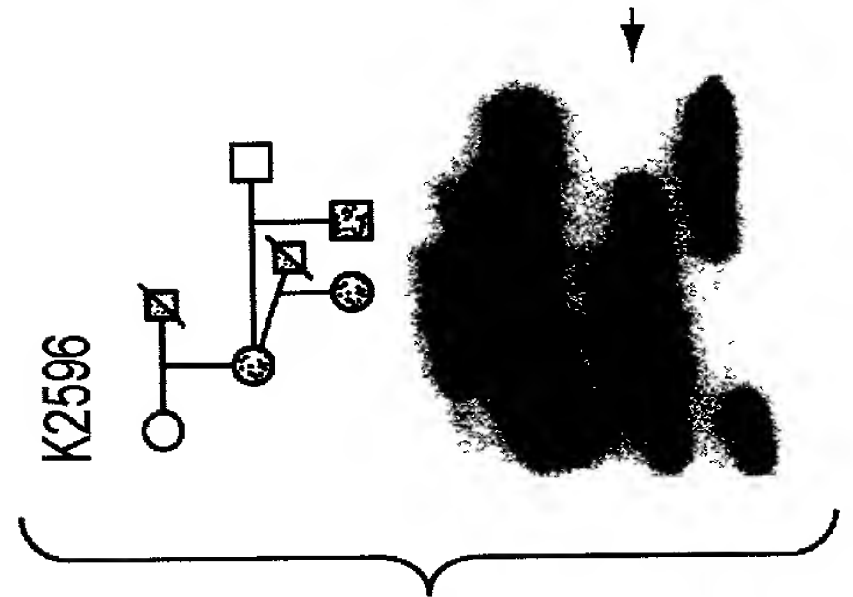
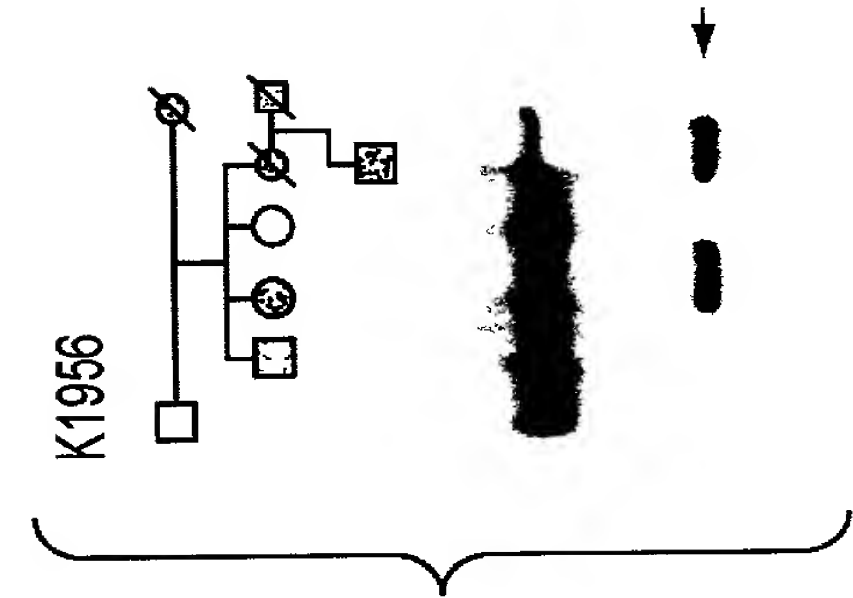


FIG. 11B



	GTG → V	SEQ ID
	GCG	NO:
	\\	
	L I A H W L	102
	↔S5↔	
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

FIG. 12G

	GAC → D	SEQ ID
	AAC	NO:
	\\	
	D I L I N F R	108
	↔S2↔	
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

5' -CAT CCT GG // gtatggg-3'

c ↓

FIG. 12H

FIG. 12I

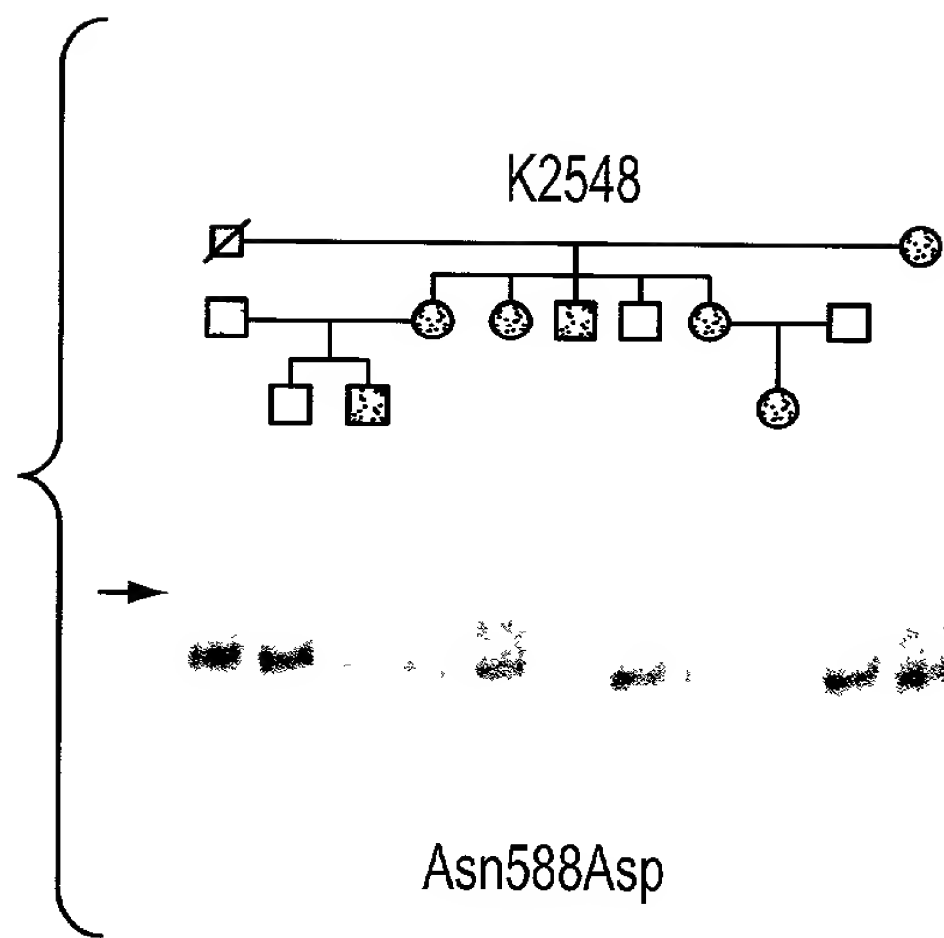


FIG. 13A



FIG. 13B

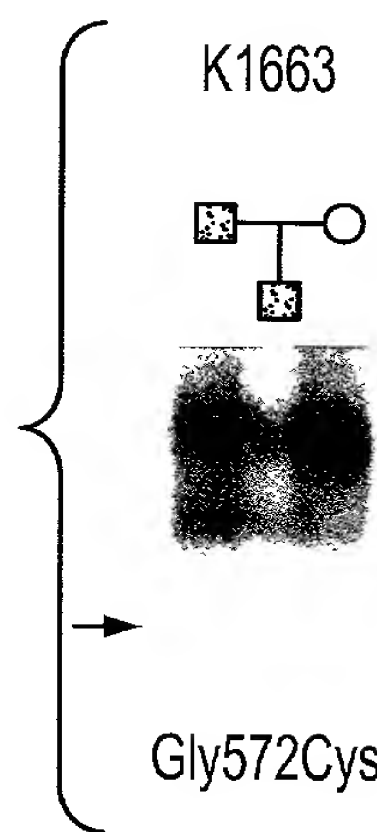


FIG. 13C

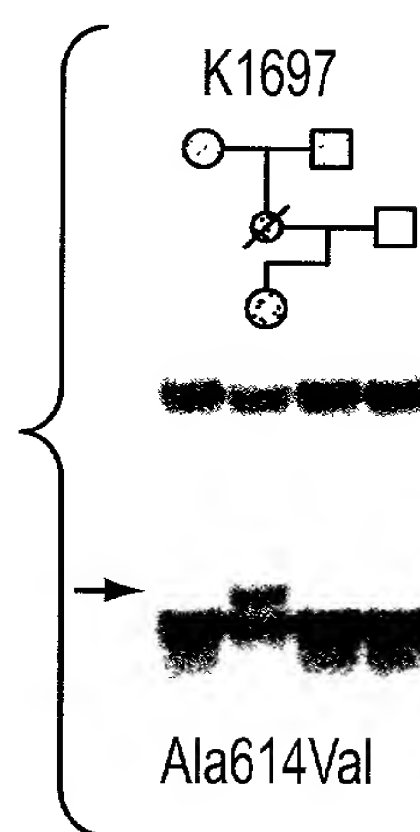


FIG. 13D

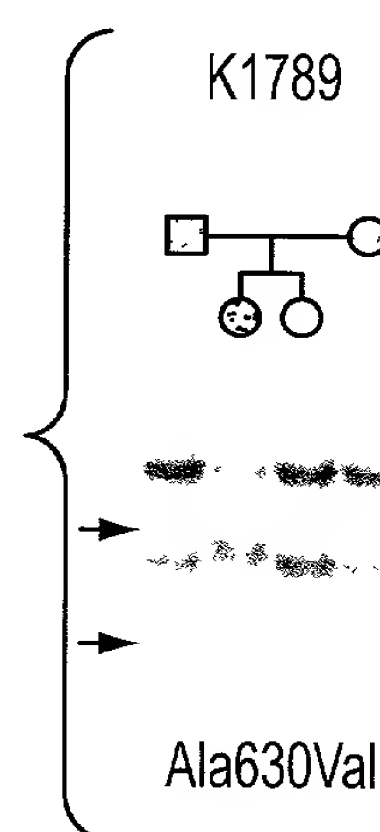


FIG. 13E

004727-5655E260

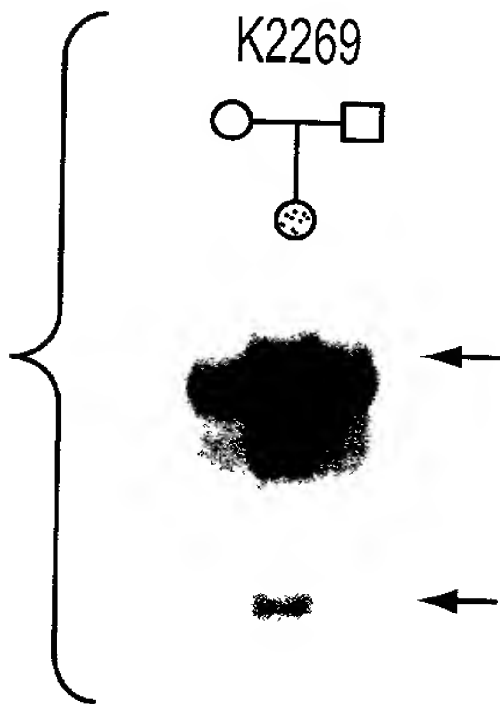


FIG. 14A

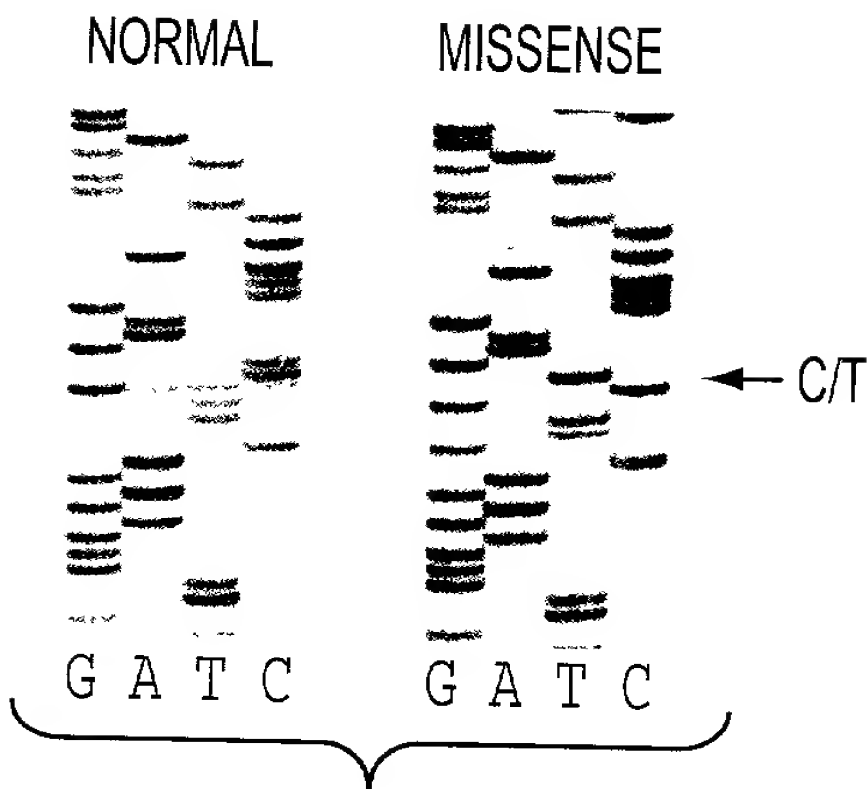


FIG. 14B

{					AGC → S				SEQ ID				
					GGC				NO:				
					↙								
					S	V	G	F	G	N	V	S	112
					←				PORE			→	
	K2269	S	V	G	F	S	N	V	S			113	
	H-Erg	S	V	G	F	G	N	V	S			112	
	M-Eag	S	V	G	F	G	N	I	A			114	
	R-Eag	S	V	G	F	G	N	I	A			114	
	Eag	S	V	G	F	G	N	V	A			115	
	Elk	S	V	G	F	G	N	V	S			112	
	Shaker	T	V	G	Y	G	D	M	T			116	

FIG. 11C

FIG. 14C

004700-13400
003500-13400

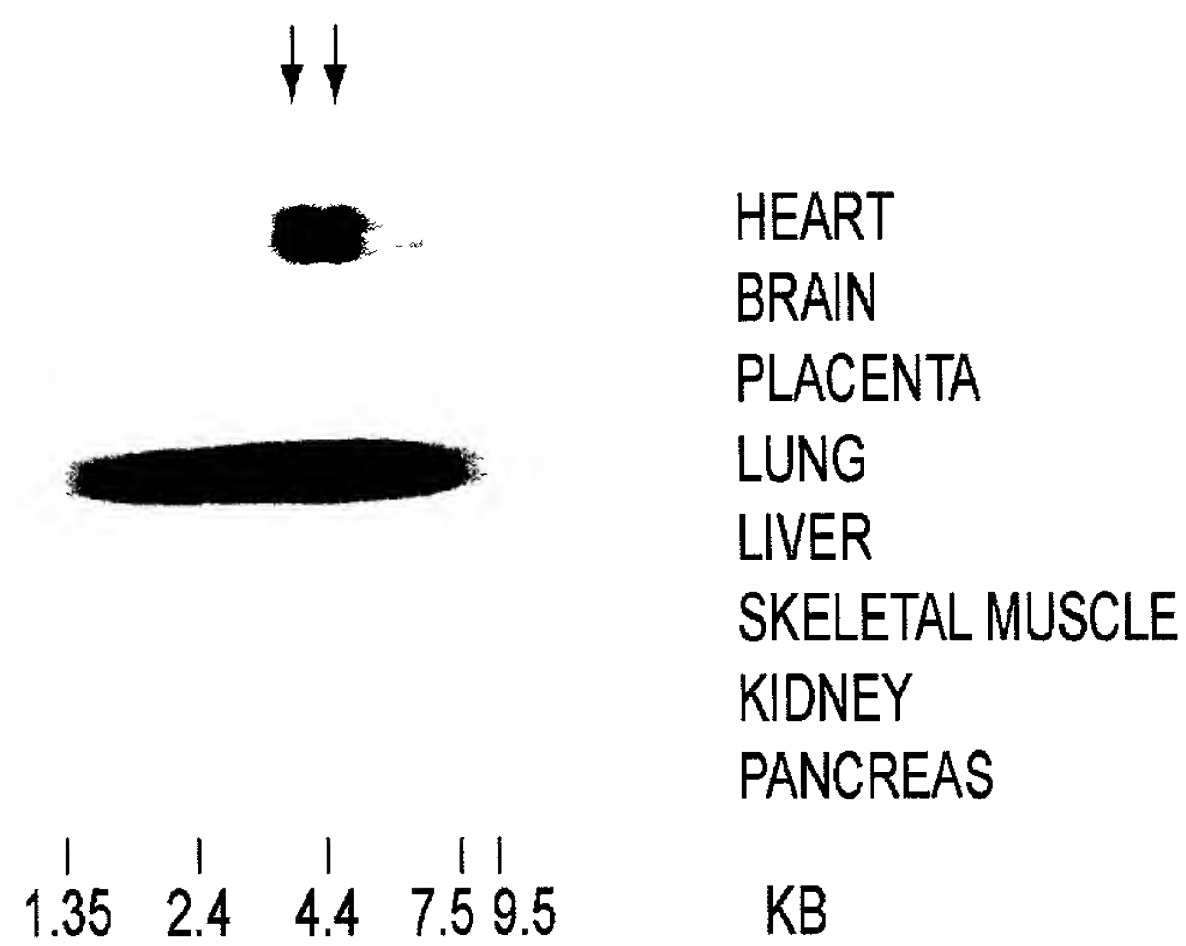


FIG. 15